

SEQUENCE LISTING

<110> Geigenberger, Peter
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 van Dongen, Joost T.
 Udvardi, Michael

<120> METHOD FOR ALTERING THE CONTENT OF RESERVE SUBSTANCES IN PLANTS

<130> 13311-00008-US

<150> PCT/EP2003/014774

<151> 2003-12-23

<150> DE 102 60 707.9

<151> 2002-12-23

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<170> PatentIn version 3.3

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<220>

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aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt	96
Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val	
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ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag	144
Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys	
35 40 45	

gag tct ggg cct aag cat agt cct cag ctc cag gcc cat gct gaa aag	192
Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys	
50 55 60	

gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga	240
Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly	
65 70 75 80	

gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa	288
Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys	
85 90 95	

gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa 336
 Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
 100 105 110

aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc 384
 Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
 115 120 125

acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag 432
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gca atg ggt taa 444
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 35 40 45

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
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Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
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Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
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Ala Met Gly
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gta	gtg	aag	tct	tgg	agt	gtc	atg	aag	aaa	aac	tca	gct	gaa	tta	ggc	96
Val	Val	Lys	Ser	Trp	Ser	Val	Met	Lys	Lys	Asn	Ser	Ala	Glu	Leu	Gly	
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ctc	aaa	ctc	ttc	atc	aag	atc	ttt	gag	att	gca	cca	aca	acg	aag	aag	144
Leu	Lys	Leu	Phe	Ile	Lys	Ile	Phe	Glu	Ile	Ala	Pro	Thr	Thr	Lys	Lys	
		35					40					45				

atg	ttc	tct	ttc	ttg	aga	gac	tca	cca	att	cct	gct	gag	caa	aat	cca	192
Met	Phe	Ser	Phe	Leu	Arg	Asp	Ser	Pro	Ile	Pro	Ala	Glu	Gln	Asn	Pro	
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aag	ctc	aag	cct	cac	gca	atg	tct	gtt	ttt	gtc	atg	tgt	tgt	gaa	tca	240
Lys	Leu	Lys	Pro	His	Ala	Met	Ser	Val	Phe	Val	Met	Cys	Cys	Glu	Ser	
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Ala	Val	Gln	Leu	Arg	Lys	Thr	Gly	Lys	Val	Thr	Val	Arg	Glu	Thr	Thr	
			85						90					95		

ttg	aag	aga	ctt	gga	gcc	agc	cat	tct	aaa	tac	ggc	gtc	gtt	gac	gaa	336
Leu	Lys	Arg	Leu	Gly	Ala	Ser	His	Ser	Lys	Tyr	Gly	Val	Val	Asp	Glu	
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cac	ttt	gag	gtg	gcc	aag	tat	gca	ttg	ttg	gag	acg	ata	aag	gag	gca	384
His	Phe	Glu	Val	Ala	Lys	Tyr	Ala	Leu	Leu	Glu	Thr	Ile	Lys	Glu	Ala	
		115					120					125				

gtg	ccg	gag	atg	tgg	tca	ccg	gag	atg	aag	gtg	gct	tgg	ggc	cag	gct	432
Val	Pro	Glu	Met	Trp	Ser	Pro	Glu	Met	Lys	Val	Ala	Trp	Gly	Gln	Ala	
	130					135					140					

tat	gat	cac	ctt	gtt	gct	gcc	att	aaa	gct	gaa	atg	aat	ctt	tcc	aac	480
Tyr	Asp	His	Leu	Val	Ala	Ala	Ile	Lys	Ala	Glu	Met	Asn	Leu	Ser	Asn	
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taa																483
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Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
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Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
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Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
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Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
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Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
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His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
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Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
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tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc      96
Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe
          20          25          30

ttc tca cag ata ctg gag ata gca cca gca gca aaa ggc ttg ttc tct      144
Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser
          35          40          45

ttc cta aga gac tca gat gaa gtc cct cac aac aat cct aaa ctc aaa      192
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gct cat gct gtt aaa gtc ttc aag atg aca tgt gaa aca gct ata cag 240
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 85 90 95

tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag 336
 Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
 100 105 110

gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag 384
 Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
 115 120 125

aaa tac aat gaa gaa gtg gaa ggt gct tgg tct caa gct tat gat cac 432
 Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
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 35 40 45

Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
 50 55 60

Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
 65 70 75 80

Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
 85 90 95

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
 100 105 110

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
 115 120 125

Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His

130

135

140

Leu Ala Leu Ala Ile Lys Thr Glu Met Lys Gln Glu Glu Ser
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NAE 737/02 PCT
MAX-PLANCK-GESSELLSCHAFT

10/540063

22.12.2003

JC20 Rec'd PCT/PTO 22 JUN 2005

SEQUENCE LISTING

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<120> Method for modifying the storage reserve content in plants

<130> NAE 737/02 PCT

<150> DE 10260707.9

<151> 2002-12-23

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aca ttc aag aaa aac ctt cct acc aac agt gtt ttg ttc tac acc gtt

96

Thr Phe Lys Lys Asn Leu Pro Thr Asn Ser Val Leu Phe Tyr Thr Val

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ata ttg gag ata gca cca act gca aaa gac atg ttc tcc ttt cta aag
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Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys
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gag tct ggg cct aag cat agt cct cag ctc cag gcc cat gct gaa aag
192

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys
50 55 60

gtt ttt gca ctg act cgt gat gct gcc act caa ctc gta gca aaa gga
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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly
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gaa gtg aca ctt gca gat gcc agc tta ggt gct gtc cac gtt cag aaa
288

Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys
85 90 95

gcc gtt act gat cct cat ttc gtg gtg gtt aaa gaa gcc ctg ctt caa
336

Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
100 105 110

aca gta aag gaa gca gtt ggg gcg gac gaa tgg agt gat gac ttg agc
384

Thr Val Lys Glu Ala Val Gly Ala Asp Glu Trp Ser Asp Asp Leu Ser
115 120 125

acc gct tgg gaa gga gca tat gat gga cta gca act gca att aag aag
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gca atg ggt taa

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Ala Met Gly

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20 25 30

Ile Leu Glu Ile Ala Pro Thr Ala Lys Asp Met Phe Ser Phe Leu Lys

35 40 45

Glu Ser Gly Pro Lys His Ser Pro Gln Leu Gln Ala His Ala Glu Lys

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Val Phe Ala Leu Thr Arg Asp Ala Ala Thr Gln Leu Val Ala Lys Gly

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Glu Val Thr Leu Ala Asp Ala Ser Leu Gly Ala Val His Val Gln Lys

85 90 95

Ala Val Thr Asp Pro His Phe Val Val Val Lys Glu Ala Leu Leu Gln
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Ala Met Gly
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gta gtg aag tct tgg agt gtc atg aag aaa aac tca gct gaa tta ggt
96

Val Val Lys Ser Trp Ser Val Met Lys Lys Asn Ser Ala Glu Leu Gly
20 25 30

ctc aaa ctc ttc atc aag atc ttt gag att gca cca aca acg aag aag
144

Leu Lys Leu Phe Ile Lys Ile Phe Glu Ile Ala Pro Thr Thr Lys Lys
35 40 45

atg ttc tct ttc ttg aga gac tca cca att cct gct gag caa aat cca
192

Met Phe Ser Phe Leu Arg Asp Ser Pro Ile Pro Ala Glu Gln Asn Pro
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288

Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
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Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
100 105 110

cac ttt gag gtg gcc aag tat gca ttg ttg gag acg ata aag gag gca
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gtg ccg gag atg tgg tca ccg gag atg aag gtg gct tgg ggt cag gct
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Val Pro Glu Met Trp Ser Pro Glu Met Lys Val Ala Trp Gly Gln Ala
130 135 140

tat gat cac ctt gtt gct gcc att aaa gct gaa atg aat ctt tcc aac
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35 40 45

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50 55 60

Lys Leu Lys Pro His Ala Met Ser Val Phe Val Met Cys Cys Glu Ser
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Ala Val Gln Leu Arg Lys Thr Gly Lys Val Thr Val Arg Glu Thr Thr
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Leu Lys Arg Leu Gly Ala Ser His Ser Lys Tyr Gly Val Val Asp Glu
 100 105 110

His Phe Glu Val Ala Lys Tyr Ala Leu Leu Glu Thr Ile Lys Glu Ala
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tcg tgg gag ata ctg aaa caa gac atc ccc aaa tac agc ctt cac ttc

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Ser Trp Glu Ile Leu Lys Gln Asp Ile Pro Lys Tyr Ser Leu His Phe

20 25 30

ttc tca cag ata ctg gag ata gca cca gca gca aaa ggc ttg ttc tct

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Phe Ser Gln Ile Leu Glu Ile Ala Pro Ala Ala Lys Gly Leu Phe Ser

35 40 45

ttc cta aga gac tca gat gaa gtc cct cac aac aat cct aaa ctc aaa

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Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys

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gct cat gct gtt aaa gtc ttc aag atg aca tgt gaa aca gct ata cag

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Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln

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ctg agg gag gaa gga aag gtg gta gtg gct gac aca acc ctc caa tat

288

Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr

85 90 95

tta ggc tca att cat ctc aaa agc ggc gtt att gac cct cac ttc gag

336

Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu

100 105 110

gtg gtg aaa gaa gct ttg cta agg aca ttg aaa gag ggg ttg ggg gag
384

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
115 120 125

aaa tac aat gaa gaa gtg gaa ggt gct tgg tct caa gct tat gat cac
432

Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
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35 40 45

Phe Leu Arg Asp Ser Asp Glu Val Pro His Asn Asn Pro Lys Leu Lys
50 55 60

Ala His Ala Val Lys Val Phe Lys Met Thr Cys Glu Thr Ala Ile Gln
65 70 75 80

Leu Arg Glu Glu Gly Lys Val Val Val Ala Asp Thr Thr Leu Gln Tyr
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Leu Gly Ser Ile His Leu Lys Ser Gly Val Ile Asp Pro His Phe Glu
100 105 110

Val Val Lys Glu Ala Leu Leu Arg Thr Leu Lys Glu Gly Leu Gly Glu
115 120 125

Lys Tyr Asn Glu Glu Val Glu Gly Ala Trp Ser Gln Ala Tyr Asp His
130 135 140

Leu Ala Leu Ala Ile Lys Thr Glu Met Lys Gln Glu Glu Ser
145 150 155